SLID
TAMY #8

ENTERED   PCT

RAW SEQUENCE LISTING   DATE: 12/26/2002
PATENT APPLICATION: **US/10/070,489A**   TIME: 13:38:55

Input Set : **A:\pto.vsk.txt**
Output Set: **N:\CRF4\12262002\J070489A.raw**

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   3 <110> APPLICANT: Glare, Travis T
   4        Hurst, Mark R H
   5        Jackson, Trevor A
   7 <120> TITLE OF INVENTION: Insecticidal Nucleotide Sequences
  10 <130> FILE REFERENCE: 24747-1104US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/070,489A
C--> 13 <141> CURRENT FILING DATE: 2002-09-17
  15 <150> PRIOR APPLICATION NUMBER: PCT/NZ00/00174
  16 <151> PRIOR FILING DATE: 2000-09-04
  18 <150> PRIOR APPLICATION NUMBER: NZ 337610
  19 <151> PRIOR FILING DATE: 1999-09-02
  21 <160> NUMBER OF SEQ ID NOS: 6
  23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
  25 <210> SEQ ID NO: 1
  26 <211> LENGTH: 18937
  27 <212> TYPE: DNA
  28 <213> ORGANISM: Serratia entomophila
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  32 <222> LOCATION: (2411)...(9547)
  33 <223> OTHER INFORMATION: SepA
  35 <221> NAME/KEY: CDS
  36 <222> LOCATION: (9598)...(13884)
  37 <223> OTHER INFORMATION: SepB ·
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  40 <222> LOCATION: (14546)...(17467)
  41 <223> OTHER INFORMATION: SepC
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  45 <223> OTHER INFORMATION: ORF1
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  48 <222> LOCATION: (13908)...(14483)
  49 <223> OTHER INFORMATION: ORF2
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  53 <223> OTHER INFORMATION: MINIMUM SEQUENCE REQUIRED FOR PATHOGENICITY AS
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  59 acatacccag tgccgataaa ctgtgacgaa cactatcaaa gatgtgttcc gtcgacctga 180
  60 aagccaggat ttatttttac accaatggtt gggtgggctt cctttctgaa ctggtgcatc 240
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 62 agttgatgac ctgctccgtg agttgaaatg ccgacggggg aaatcagcag cctttttcaac 360
 63 tcatggagca gggggaaatc aatcctcaat aacccgcatt ggatatcctg ccagtgtgca 420
 64 tttaaccttt ttagtgtgtt tccttaatat cccaatcgtt gaatcgctac atacggcaga 480
 65 cattagtatc tcacttatca tcaaagtaat atcacaccga gaatgctaat ttcatgatat 540
 66 gaaaacgttc cattaataaa ttttcagaaa cctaacacgg cattttatg ctgatcagtg 600
 67 aattgattgt ttctgaaaaa attaattgca cctctgccac ttatcagata aaaacacccc 660
 68 atgcggtaag tttttattt tttattaatg attttattaa tgattttatt aatgatttta 720
 69 ttaatgattt tattaatgat tttactatag atgaatgtta acatgggtga taatttactt 780
 70 tactcaattt aattgttggt atgaccatgt tttagatgag tggcacggat tcattattgt 840
 71 aaaaaaagta tctaaaacct ttagcagcaa tcctacttga ggatgacctc gacaggactt 900
 72 gattattgcc attttttacg aaggaagatg acgggtgata aataataaaa aaaacaaaag 960
 73 tatagcctta ggtatcgccg attacatcca gtaacactta ttgacttttt tttacttcta 1020
 74 ccgttagcta taaatatgat atttaaatct gtatttttat ataaaaccag tttatgatgc 1080
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 77 gttgctttga tgttaaatta acgtgttcat tcattatgtt ctactgttgt ttctattgtc 1260
 78 cggaacgacc atagagactg tcgctatgtt aataggaata tttgactggt tatatgcgcc 1320
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 85 aaaaacattg tcgtctcttt tattgctttt ctcattatta cggcgtgcgg cgctgtctcc 1740
 86 atcaggacga tgacggggga gtattactat gcggattggt ccgagacgat cattaacctt 1800
 87 tcgcttttcc tgtctgttta tatacgcaat ggcgaaatcc ttcggtgggg ggagaaaaa 1859
 88 atg aag ata agt tcc cga ggt atc gca tta atc aaa gag ttc gaa ggt 1907
 89 Met Lys Ile Ser Ser Arg Gly Ile Ala Leu Ile Lys Glu Phe Glu Gly
 90   1               5                  10                  15
 92 ctg cgc tta cac gct tat cgc tgc gcc gct gac gtc tgg act gtc ggt 1955
 93 Leu Arg Leu His Ala Tyr Arg Cys Ala Ala Asp Val Trp Thr Val Gly
 94             20                  25                  30
 96 tat ggc cac acg gca ggg gtt aca aag ggt gac atc atc acg gtc gat 2003
 97 Tyr Gly His Thr Ala Gly Val Thr Lys Gly Asp Ile Ile Thr Val Asp
 98             35                  40                  45
100 gaa gcc cag acg atg ctg aca aac gat att acc gta ttt gaa cgg gcg 2051
101 Glu Ala Gln Thr Met Leu Thr Asn Asp Ile Thr Val Phe Glu Arg Ala
102         50                  55                  60
104 gtc agt cag gcc gtc gcg gtt cct ctg aat cag tcg caa tac gat gcc 2099
105 Val Ser Gln Ala Val Ala Val Pro Leu Asn Gln Ser Gln Tyr Asp Ala
106 65                  70                  75                  80
108 ctg gtt tct ttg gtt ttt aat att ggc cag ggg aat ttt aaa cgc tct 2147
109 Leu Val Ser Leu Val Phe Asn Ile Gly Gln Gly Asn Phe Lys Arg Ser
110                 85                  90                  95
112 acc ttg ttg aaa aaa ctc aac aaa cag gac tat gtc ggc gcc ggg aac 2195
113 Thr Leu Leu Lys Lys Leu Asn Lys Gln Asp Tyr Val Gly Ala Gly Asn
114                 100                 105                 110
116 gag ttt tta cgc tgg acc cgg gcc aat ggg aag gtc ctt ccc gga ctg 2243
117 Glu Phe Leu Arg Trp Thr Arg Ala Asn Gly Lys Val Leu Pro Gly Leu
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118         115                  120                  125
120 att cgc cga cgc gaa gct gaa cgg gtg ttg ttt gag aaa ctg ggt gca    2291
121 Ile Arg Arg Arg Glu Ala Glu Arg Val Leu Phe Glu Lys Leu Gly Ala
122      130                  135                  140
124 taa ccctttgcga cgtacccaca agatgaagat aacaccgcgt actgagcggt         2344
125  *
W--> 128 ggcgcaacaa tgaataaatg actgtgtacg gcctgtcctt cacaacggat gggaccatca 2404
129 acgtaa tga atg agg caa gac att atg tat aat att gat gat att ctg      2452
130         *  Met Arg Gln Asp Ile Met Tyr Asn Ile Asp Asp Ile Leu
131             145                  150                  155
133 gag aaa gtg aat gct cca cga gca cgc ctg tca gaa gaa aac gat aca    2500
134 Glu Lys Val Asn Ala Pro Arg Ala Arg Leu Ser Glu Glu Asn Asp Thr
135      160                  165                  170
137 gcg gtg acg ctg acg gat tta ttc tcg cgt tcg ttt ccc gag gtc aaa    2548
138 Ala Val Thr Leu Thr Asp Leu Phe Ser Arg Ser Phe Pro Glu Val Lys
139      175                  180                  185
141 aaa atc act ggc gac agc ctg tca tgg gga gag gtc tgc tat ctg tac    2596
142 Lys Ile Thr Gly Asp Ser Leu Ser Trp Gly Glu Val Cys Tyr Leu Tyr
143 190                  195                  200                  205
145 agt cag gcg cag cac gaa cag aaa gaa aac cgg ctc acc gaa tcc cgt    2644
146 Ser Gln Ala Gln His Glu Gln Lys Glu Asn Arg Leu Thr Glu Ser Arg
147                  210                  215                  220
149 att ctg gcc cgg gcg aat ccc cta ctg gtg aat gcc gtt cgc ctg gga    2692
150 Ile Leu Ala Arg Ala Asn Pro Leu Leu Val Asn Ala Val Arg Leu Gly
151                  225                  230                  235
153 ata cgg cag gca gcc ggc agt cgc agc tat gat gac tgg ttt ggc tcc    2740
154 Ile Arg Gln Ala Ala Gly Ser Arg Ser Tyr Asp Asp Trp Phe Gly Ser
155                  240                  245                  250
157 cgc gca gac cgt ttc gcc cgc ccc ggc tcg gtg gcc tcc atg ttc tca    2788
158 Arg Ala Asp Arg Phe Ala Arg Pro Gly Ser Val Ala Ser Met Phe Ser
159      255                  260                  265
161 ccg gcg gcg tat ctg acc gag ctg tac cgt gag gcg aag gac ctg cat    2836
162 Pro Ala Ala Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Lys Asp Leu His
163 270                  275                  280                  285
165 ccg gac acc tcg ctg ttc cgg ctg gac atc cgg cgt ccc gac ctg gcg    2884
166 Pro Asp Thr Ser Leu Phe Arg Leu Asp Ile Arg Arg Pro Asp Leu Ala
167                  290                  295                  300
169 gcg ctg gcc ctt agc cag aat aat atg gac gac gag ctc tcc acc ctg    2932
170 Ala Leu Ala Leu Ser Gln Asn Asn Met Asp Asp Glu Leu Ser Thr Leu
171                  305                  310                  315
173 agc ctg tcc aat gag cta ctg tat cgc ggt atc ggg gca gcg gaa ggg    2980
174 Ser Leu Ser Asn Glu Leu Leu Tyr Arg Gly Ile Gly Ala Ala Glu Gly
175           320                  325                  330
177 ctt gac gac gac agc gtc agg gag ctg ctc gcc ggg tat cgc ctg acc    3028
178 Leu Asp Asp Asp Ser Val Arg Glu Leu Leu Ala Gly Tyr Arg Leu Thr
179      335                  340                  345
181 ggc ctg acc ccc tat cac tgg gcg tac gag gcg gcc cgc caa gcc att    3076
182 Gly Leu Thr Pro Tyr His Trp Ala Tyr Glu Ala Ala Arg Gln Ala Ile
183 350                  355                  360                  365
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186 Leu Val Gln Asp Pro Thr Leu Met Gly Phe Ser Arg Asn Pro Asp Val
187             370             375                 380
189 gcg cag ctt atg gac cct gcc tcc atg ctg gcc att gaa gcc gat att   3172
190 Ala Gln Leu Met Asp Pro Ala Ser Met Leu Ala Ile Glu Ala Asp Ile
191             385             390                 395
193 tca ccg gag ctg tat cag ata ctg gcc gaa gaa att acg aca gac agt   3220
194 Ser Pro Glu Leu Tyr Gln Ile Leu Ala Glu Glu Ile Thr Thr Asp Ser
195         400             405                 410
197 tac gaa gca ctc tgg agt aag aat ttt ggt gat atg cct ccc tcc tca   3268
198 Tyr Glu Ala Leu Trp Ser Lys Asn Phe Gly Asp Met Pro Pro Ser Ser
199     415             420                 425
201 ctg tta tct tat gat gca ctt gca aca ttt tat gat ctt gat tac gat   3316
202 Leu Leu Ser Tyr Asp Ala Leu Ala Thr Phe Tyr Asp Leu Asp Tyr Asp
203 430                 435             440                 445
205 gag cta act tcg tta ttg tca tta agg ctg gac ttt tca aat cca aac   3364
206 Glu Leu Thr Ser Leu Leu Ser Leu Arg Leu Asp Phe Ser Asn Pro Asn
207                 450             455                 460
209 aat gaa tac tac att aat agt caa tta agt gtc gta act ctg aat gaa   3412
210 Asn Glu Tyr Tyr Ile Asn Ser Gln Leu Ser Val Val Thr Leu Asn Glu
211             465             470                 475
213 agc act ggt tta ata act ata cat cat tat tta aga acg cta ggc gga   3460
214 Ser Thr Gly Leu Ile Thr Ile His His Tyr Leu Arg Thr Leu Gly Gly
215             480             485                 490
217 gac tca cag cag att aac cct gag ctt ata cct tat ggg gat gga aca   3508
218 Asp Ser Gln Gln Ile Asn Pro Glu Leu Ile Pro Tyr Gly Asp Gly Thr
219     495             500                 505
221 tat ctt tat aat ttc agc gtg gtg tca acg ata tca gag gat agt ttc   3556
222 Tyr Leu Tyr Asn Phe Ser Val Val Ser Thr Ile Ser Glu Asp Ser Phe
223 510             515                 520                 525
225 aaa cta ggg tcg tta ggt tct aac agt agc aat ctt tac tct ggg gat   3604
226 Lys Leu Gly Ser Leu Gly Ser Asn Ser Ser Asn Leu Tyr Ser Gly Asp
227             530             535                 540
229 tat cag ctt caa aaa ggg gtt cgc tat agc att cct gtt gaa ata gat   3652
230 Tyr Gln Leu Gln Lys Gly Val Arg Tyr Ser Ile Pro Val Glu Ile Asp
231             545             550                 555
233 gaa gga aag tta aat gat ggg atc aca ata gga ttg agt agg aaa ggg   3700
234 Glu Gly Lys Leu Asn Asp Gly Ile Thr Ile Gly Leu Ser Arg Lys Gly
235             560             565                 570
237 ggg gga tat tac tca aca gta aac ttc act ctg att gaa tat gat cct   3748
238 Gly Gly Tyr Tyr Ser Thr Val Asn Phe Thr Leu Ile Glu Tyr Asp Pro
239     575             580                 585
241 gcg ata ttc att ctt aaa tta aat aaa gtt atc cgc cta tac aag gcc   3796
242 Ala Ile Phe Ile Leu Lys Leu Asn Lys Val Ile Arg Leu Tyr Lys Ala
243 590             595                 600                 605
245 acg ggc atg acc acg gcg gaa ata tat caa atc acc aat att ctt aat   3844
246 Thr Gly Met Thr Thr Ala Glu Ile Tyr Gln Ile Thr Asn Ile Leu Asn
247             610             615                 620
249 aac ggt ctc acc att gac cat gcg gtc ctg agt aaa atc ttc ctg gtc   3892
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Input Set : **A:\pto.vsk.txt**
Output Set: **N:\CRF4\12262002\J070489A.raw**

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250 Asn Gly Leu Thr Ile Asp His Ala Val Leu Ser Lys Ile Phe Leu Val
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253 cgt tac ctg atg cgt cac tat cag ctt gat gtg gcc cgg tca ctg ata    3940
254 Arg Tyr Leu Met Arg His Tyr Gln Leu Asp Val Ala Arg Ser Leu Ile
255         640             645             650
257 ttg tgc aac gga acc atc agt gac cag gcg ttc agc ggc gaa acc ggc    3988
258 Leu Cys Asn Gly Thr Ile Ser Asp Gln Ala Phe Ser Gly Glu Thr Gly
259     655             660             665
261 ctg ttc acc acg ctg ttc aac acc cca ccg ctg aac ggc cag ctg ttt    4036
262 Leu Phe Thr Thr Leu Phe Asn Thr Pro Pro Leu Asn Gly Gln Leu Phe
263 670             675             680             685
265 tct gca gat gat acc ccc ctc gac tta cgc tct gaa gca ccg gag gat    4084
266 Ser Ala Asp Asp Thr Pro Leu Asp Leu Arg Ser Glu Ala Pro Glu Asp
267             690             695             700
269 gct ttc cgt ctc agc gta ctg aaa cgc gca ttt aac atc agc gcc tcg    4132
270 Ala Phe Arg Leu Ser Val Leu Lys Arg Ala Phe Asn Ile Ser Ala Ser
271             705             710             715
273 ggg ctt tcc acg ctc tgg cag ttg gcc agc ggt gac agc agc gct ggg    4180
274 Gly Leu Ser Thr Leu Trp Gln Leu Ala Ser Gly Asp Ser Ser Ala Gly
275         720             725             730
277 ttt agc tgc tct gct gac aat atc gcc gca ctc tac cga gtg aaa ctc    4228
278 Phe Ser Cys Ser Ala Asp Asn Ile Ala Ala Leu Tyr Arg Val Lys Leu
279     735             740             745
281 ctg gct gac atc cac gac cta tcc gct ggt gag ctg tca atg ttg ctg    4276
282 Leu Ala Asp Ile His Asp Leu Ser Ala Gly Glu Leu Ser Met Leu Leu
283 750             755             760             765
285 tcc gtc tcc cct ttc agc ggg gtg gcc gcc ggc tcg ctg tcc gat aat    4324
286 Ser Val Ser Pro Phe Ser Gly Val Ala Ala Gly Ser Leu Ser Asp Asn
287             770             775             780
289 gag ctg acg cag ttt ctg tac cag acc acc acc tgg ctc acg gag cag    4372
290 Glu Leu Thr Gln Phe Leu Tyr Gln Thr Thr Thr Trp Leu Thr Glu Gln
291             785             790             795
293 ggc tgg acg gtc agc gat gtg ttc ctg atg ctg acg acg cag tac ggt    4420
294 Gly Trp Thr Val Ser Asp Val Phe Leu Met Leu Thr Thr Gln Tyr Gly
295         800             805             810
297 acc ctg ctg acc ccc gac att gag aac ctg ctc gct tcc ctg cgc aac    4468
298 Thr Leu Leu Thr Pro Asp Ile Glu Asn Leu Leu Ala Ser Leu Arg Asn
299     815             820             825
301 gga ctg tcg ggc cgt gag ctg ttc ccg gaa acg ctc ccc ggc gat ggc    4516
302 Gly Leu Ser Gly Arg Glu Leu Phe Pro Glu Thr Leu Pro Gly Asp Gly
303 830             835             840             845
305 gct ccc ttt att gcc gcc gcc atg cag ctg gac gcc acg gat acg gcg    4564
306 Ala Pro Phe Ile Ala Ala Ala Met Gln Leu Asp Ala Thr Asp Thr Ala
307             850             855             860
309 aag gcg atg ctg act tgg gcg gac cag ttg aag cca gag ggg ctg acg    4612
310 Lys Ala Met Leu Thr Trp Ala Asp Gln Leu Lys Pro Glu Gly Leu Thr
311             865             870             875
313 ctg acg gaa ttt att ctt ttg gtg atg aat gcc gcc cca aat gac gag    4660
314 Leu Thr Glu Phe Ile Leu Leu Val Met Asn Ala Ala Pro Asn Asp Glu
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VERIFICATION SUMMARY   DATE: 12/26/2002
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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:39 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:43 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:47 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:51 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:56 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:128 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1